5th Scottish Chromatin Group meeting

www.scottishchromatin.co.uk

Thursday 23rd October 2008, 2-6 pm

SLT, Wellcome Trust Biocentre, University of Dundee

Frank Pugh Pennsylvania

Genomic organization of chromatin and the transcription machinery

Ana Pombo *London*

Transcription complexes in epigenetics and genome function

Daimark Bennett Liverpool

Epigenetic regulation by Protein Phosphatase 1 in Drosophila

David Lleres Dundee

Quantitative Analysis of Chromatin Higher-Order Organization by FRET-FLIM in living cells

Researchers and students from across Scotland are welcome

No registration required - Refreshments provided

Scottish Chromatin Group

The Fifth Scottish Chromatin Group Meeting, University of Dundee, College of Life Sciences, SLT.

Programme

1400 -1445 **Dr. Ana Pombo, London.**

"Transcription complexes in epigenetics and genome function"

Ana's research has contributed to understanding the functional compartmentalisation of the genome within the mammalian cell nucleus and to unravel novel functional properties of RNA polymerase II complexes. She is currently studying the regulation and functions of poised polymerases in epigenetic regulation of gene expression and genome organisation, investigating 3D genome architecture relative to functional and structural nuclear landmarks in mammalian systems with a specific interest in stochastic processes, and characterizing the proteome of RNA polymerase II complexes.

Recent Publications:

- Ring1-mediated ubiquitination of H2A restrains poised RNA polymerase II at bivalent genes in mouse ES cells. Nat Cell Biol. 2007 9:1428-35.
- Intermingling of chromosome territories in interphase suggests role in translocations and transcription-dependent associations. PLoS Biol. 2006 4:e138.

1445 - 1515 Dr Daimark Bennett, Liverpool.

"Epigenetic regulation by Protein Phosphatase 1 in /Drosophila/"

1515 - 1615 Break – tea / coffee in atrium

1615 – 1730 Dr. Frank Pugh, Pennsylvania.

"Genomic organization of chromatin and the transcription machinery"

A genome-wide understanding of gene regulation requires a detailed knowledge of where nucleosomes, their regulators, and components of the transcription machinery reside in relation to each other. Potential mechanisms that define the remarkable uniformity by which nucleosomes are organized around genes will be presented, contrasting the patterns found in *Saccharomyces* vs *Drosophila* (and other organisms). Within this context I will report on our progress towards high resolution maps of where proteins that regulate chromatin and transcription are located, including identification of sites where RNA polymerase II is rate-limited during transcription.

Recent Publications:

- Nucleosome organization in the Drosophila genome. Nature. 2008 453:358-62.
- Translational and rotational settings of H2A.Z nucleosomes across the Saccharomyces cerevisiae genome. Nature. 2007 446:572-6

1730 – 1800 Dr. David Lleres, Lamond Lab, Dundee.

"Quantitative Analysis of Chromatin Higher-Order Organization by FRET-FLIM in living cells"

1800 – 2000 Buffet drinks reception, WTB atrium